In the Specification:

Please amend the specification as shown:

Please delete paragraph [0051] and replace it with the following paragraph:

[0051] Table 3 provides an alignment of kinase domains for several kinases, including human PYK2, providing identification of residues conserved between various members of the set **(residues 21-293 of SEQ ID NO: 2 and SEQ ID NOS 9-21, respectively, in order of appearance)**. The residue number is for PYK2.

Please delete paragraph [0260] and replace it with the following paragraph:

[0260] The target molecule can be bound to the scintillator plates by a variety of well known means. Scintillant plates are available that are derivatized to bind to fusion proteins such as GST, His6 **(SEQ ID NO: 22)** or Flag fusion proteins. Where the target molecule is a protein complex or a multimer, one protein or subunit can be attached to the plate first, then the other components of the complex added later under binding conditions, resulting in a bound complex.

Please delete paragraph [0366] and replace it with the following paragraph:

[0366] Kinase domain of PYK2 (amino acids 420 - 691) was amplified by polymerase chain reaction (PCR) using the specific primers 5'-TCCACAGCATATGATTGCCCGTGAAGA TGTGGT-3' (SEQ ID NO: 5) and 5'-CTCTCGTCGACCTACATGGCAATGTCCTTCTCCA-3' (SEQ ID NO: 6). The resulting PCR fragment was digested with *Nde*I and *Sal*I and was ligated into a modified pET15b vector (Novagen) with a cleavable N-terminal hexa-histidine tag (designated pET1S). PYK2 coding sequence has been deposited with GenBank under accession number U33284. A desired PYK2 sequence can be obtained using PCR with a brain (*e.g.*, human brain) cDNA library, such as obtaining kinase domain using the above primers in PCR. The multi-cloning site of the pET15S vector is shown in the following

sequence (SEQ ID NO: 7), including the sequence encoding the N-terminal hexa-histadine tag **(peptide shown in SEQ ID NO: 8)**:

T7 promoter
AGATCTCGATCCCGCGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCC

RBS
TCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACC

NdeI
ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGC**CATATG**GGATCCGG
M G S S H H H H H H S S G L V P R G S H M --------

StuI **SalI**
AATTCAAAGGCCTAC**GTCGAC**TAGAGCCTGCAGT*CTCGA*CCATCATCATCATCATCATTAATAAAAGG[redacted]
---------- *

SpeI **BamHI**
[redacted]GGCCGTT**ACTAGT**GGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGG
IVEX-3 Primer

Bpu1102 I **T7 terminator**
CTGCTGCCACC[redacted]ACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG
3'-PET Primer

Please delete paragraph [0367] and replace it with the following paragraph:

[0367] pET15S vector is derived from pET15b vector (Novagen) for bacterial expression to produce the proteins with N-terminal His6 **(SEQ ID NO: 22)**. This vector was modified by replacement of NdeI-BamHI fragment to others to create SalI site and stop codon (TAG). Vector size is 5814 bp. Insert can be put using NdeI-SalI site.

Please delete paragraph [0384] and replace it with the following paragraph:

[0384] To test whether Y402 can reach the substrate binding site, we modeled the 7 residue peptide $D^{400}IYAEIPD^{407}$ **(SEQ ID NO: 23)** containing Y^{402} into the substrate binding site based on the cocrystal structure of IGFR1 kinase domain with its substrate peptide. In our protein construct, the Pyk2 insert starts at I420. There are four residues (GSHM) **(SEQ ID NO: 24)** N-terminal to I420 left by the His-tag

used, of those only M419 is visible. We then modeled the 11 residues that link D419 to M407. The model shows that, in order to reach the substrate binding site, the N-terminal region has to transverse along the back of αC. The link would also fix the A-loop in the active conformation. This may provide the mechanism that the protein used to autophosphorylate Y402. Once Y402 is phosphorylated, the N-terminus is then released and subject to SH2 binding. The A-loop also becomes flexible and accessible to Src.

Please delete paragraph [0385] and replace it with the following paragraph:

[0385] Because the residues surrounding the P+1 and P+3 binding pocket are mostly hydrophobic in tyrosine kinases, substrate P+1 and P+3 sites are mostly hydrophobic residues. The residue that might interact with P+2 varies. Acidic and other polar site chains might be preferred because of the nearby residue R586. The P-1 site is an acidic residue in INSR and IGFR1. The residue for interacting with P-1 is Arg; this residue is changed to Gly in Pyk2, leaving the space largely hydrophobic. The autophosphorylation site sequence in Pyk2, IYAEIPD **(SEQ ID NO: 25)**, and the sequences of several other known Pyk2 phosphorylation sites fit well the substrate selectivity profile of Pyk2.